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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=12; day=18; hr=15; min=25; sec=51; ms=357;
]

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Application No: 10552949 Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-01 18:51:30.378
Finished: 2008-12-01 18:51:31.157
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 779 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

Error code	Error Description
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SEQUENCE LISTING

<110> Omary, Bishr
Ku, Nam-Om

<120> Keratin 8 and 18 mutations are Risk
Factors for Developing Liver Disease of Multiple Etiologies

<130> STAN-297WO

<140> 10552949
<141> 2008-12-01

<150> 60/462, 989
<151> 2003-04-14

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agc ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc 166
Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly
1 5 10 15

tct gtc cag gcg ccc agc tac ggc gcc cgg ccc gtc agc agc gcg gcc 214
Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala
20 25 30

agc gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc 262
Ser Val Tyr Ala Gly Ala Gly Ser Gly Ser Arg Ile Ser Val Ser
35 40 45

cgc tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc 310
Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr
50 55 60

ggg ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag 358
Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys
65 70 75 80

gag acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga 406
Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg

85	90	95	
gtg agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg			454
100	105	110	
gag cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr			502
115	120	125	
ttc aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val			550
130	135	140	
gac aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala			598
145	150	155	160
gat gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser			646
165	170	175	
gtg gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn			694
180	185	190	
atc aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu			742
195	200	205	
ctg ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln			790
210	215	220	
gcc cag att gcc agc tct ggg ttg acc gtc gag gta gat gcc ccc aaa Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys			838
225	230	235	240
tct cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp			886
245	250	255	
gag ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln			934
260	265	270	
cag att gag gag agc acc aca gtc acc aca cag tct gct gag gtt Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val			982
275	280	285	
gga gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser			1030
290	295	300	
ttg gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu			1078
305	310	315	320

aac agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag Asn Ser Leu Arg Glu Val Ala Arg Tyr Ala Leu Gln Met Glu Gln	325	330	335	1126
ctc aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg	340	345	350	1174
gca gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Ala Leu Leu Asn Ile	355	360	365	1222
aag gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu	370	375	380	1270
gat ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser	385	390	395	400
atg caa acc atc caa aag acc acc acc cgc cggtata gtg gat ggc aaa Met Gln Thr Ile Gln Lys Thr Thr Arg Arg Ile Val Asp Gly Lys	405	410	415	1366
gtg gtg tct gag acc aat gac acc aaa gtt ctg agg cat taa Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His *	420	425		1408
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20 25 30				
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35 40 45				
Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr				
50 55 60				
Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys				
65 70 75 80				
Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg				
85 90 95				
Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg				
100 105 110				
Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr				
115 120 125				
Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val				
130 135 140				
Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala				

145	150	155	160
Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser			
165	170	175	
Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn			
180	185	190	
Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu			
195	200	205	
Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln			
210	215	220	
Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys			
225	230	235	240
Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp			
245	250	255	
Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln			
260	265	270	
Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val			
275	280	285	
Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser			
290	295	300	
Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu			
305	310	315	320
Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln			
325	330	335	
Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg			
340	345	350	
Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile			
355	360	365	
Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu			
370	375	380	
Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser			
385	390	395	400
Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys			
405	410	415	
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Ser Ile Arg Val Thr Gln Lys Ser Tyr Lys Val Ser Thr Ser Gly			
1	5	10	15
ccc cgg gcc ttc agc agc cgc tcc tac acg agt ggg ccc ggt tcc cgc		155	
Pro Arg Ala Phe Ser Ser Arg Ser Tyr Thr Ser Gly Pro Gly Ser Arg			
20	25	30	
atc agc tcc tcg agc ttc tcc cga gtg ggc agc agc aac ttt cgc ggt		203	

Ile Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly			
35	40	45	
ggc ctg ggc ggc tat ggt ggg gcc agc ggc atg gga ggc atc acc			251
Gly Leu Gly Gly Tyr Gly Ala Ser Gly Met Gly Gly Ile Thr			
50	55	60	
gca gtt acg gtc aac cag agc ctg ctg agc ccc ctt gtc ctg gag gtg			299
Ala Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val			
65	70	75	
gac ccc aac atc cag gcc gtg cgc acc cag gag aag gag cag atc aag			347
Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys			
80	85	90	95
acc ctc aac aac aag ttt gcc tcc ttc ata gac aag gta cgg ttc ctg			395
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu			
100	105	110	
gag cag cag aac aag atg ctg gag acc aag tgg agc ctc ctg cag cag			443
Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln			
115	120	125	
cag aag acg gct cga agc aac atg gac aac atg ttc gag agc tac atc			491
Gln Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile			
130	135	140	
aac aac ctt agg cgg cag ctg gag act ctg ggc cag gag aag ctg aag			539
Asn Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys			
145	150	155	
ctg gag gcg gag ctt ggc aac atg cag ggg ctg gtg gag gac ttc aag			587
Leu Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys			
160	165	170	175
aac aag tat gag gat gag atc aat aag cgt aca gag atg gag aac gaa			635
Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Thr Glu Met Glu Asn Glu			
180	185	190	
ttt gtc ctc atc aag aag gat gtg gat gaa gct tac atg aac aag gta			683
Phe Val Leu Ile Lys Lys Asp Val Asp Glu Ala Tyr Met Asn Lys Val			
195	200	205	
gag ctg gag tct cgc ctg gaa ggg ctg acc gac gag atc aac ttc ctc			731
Glu Leu Glu Ser Arg Leu Glu Gly Leu Thr Asp Glu Ile Asn Phe Leu			
210	215	220	
agg cag cta tat gaa gag gag atc cgg gag ctg cag tcc cag atc tcg			779
Arg Gln Leu Tyr Glu Glu Ile Arg Glu Leu Gln Ser Gln Ile Ser			
225	230	235	
gac aca tct gtg gtg ctg tcc atg gac aac agc cgc tcc ctg gac atg			827
Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp Met			
240	245	250	255
gac agc atc att gct gag gtc aag gca cag tac gag gat att gcc aac			875
Asp Ser Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Asp Ile Ala Asn			

260	265	270	
cgc agc cgg gct gag gag agc atg tac cag atc aag tat gag gag			923
Arg Ser Arg Ala Glu Ala Glu Ser Met Tyr Gln Ile Lys Tyr Glu Glu			
275	280	285	
ctg cag agc ctg gct ggg aag cac ggg gat gac ctg cgg cgc aca aag			971
Leu Gln Ser Leu Ala Gly Lys His Gly Asp Asp Leu Arg Arg Thr Lys			
290	295	300	
act gag atc tct gag atg aac cgg aac atc agc cgg ctc cag gct gag			1019
Thr Glu Ile Ser Glu Met Asn Arg Asn Ile Ser Arg Leu Gln Ala Glu			
305	310	315	
att gag ggc ctc aaa ggc cag agg gct tcc ctg gag gcc gcc att gca			1067
Ile Glu Gly Leu Lys Gly Gln Arg Ala Ser Leu Glu Ala Ala Ile Ala			
320	325	330	335
gat gcc gag cag cgt gga gag ctg gcc att aag gat gcc aac gcc aag			1115
Asp Ala Glu Gln Arg Gly Glu Leu Ala Ile Lys Asp Ala Asn Ala Lys			
340	345	350	
ttg tcc gag ctg gag gcc gcc ctg cag cgg gcc aag cag gac atg gcg			1163
Leu Ser Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met Ala			
355	360	365	
cgg cag ctg cgt gag tac cag gag ctg atg aac gtc aag ctg gcc ctg			1211
Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu			
370	375	380	
gac atc gag atc gcc acc tac agg aag ctg ctg gag ggc gag gag agc			1259
Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser			
385	390	395	
cgg ctg gag tct ggg atg cag aac atg agt att cat acg aag acc acc			1307
Arg Leu Glu Ser Gly Met Gln Asn Met Ser Ile His Thr Lys Thr Thr			
400	405	410	415
agc ggc tat gca ggt ggt ctg agc tcg gcc tat ggg ggc ctc aca agc			1355
Ser Gly Tyr Ala Gly Gly Leu Ser Ser Ala Tyr Gly Leu Thr Ser			
420	425	430	
ccc ggc ctc agc tac agc ctg ggc tcc agc ttt ggc tct ggc gcg ggc			1403
Pro Gly Leu Ser Tyr Ser Leu Gly Ser Ser Phe Gly Ser Gly Ala Gly			
435	440	445	
tcc agc tcc ttc agc cgc acc agc tcc tcc agg gcc gtg gtt gtg aag			1451
Ser Ser Ser Phe Ser Arg Thr Ser Ser Ser Arg Ala Val Val Val Lys			
450	455	460	
aag atc gag aca cgt gat ggg aag ctg gtg tct gag tcc tct gac gtc			1499
Lys Ile Glu Thr Arg Asp Gly Lys Leu Val Ser Glu Ser Ser Asp Val			
465	470	475	
ctg ccc aag tga acagctgcgg cagccccctcc cagccctaccc ctccctgcgct			1551
Leu Pro Lys *			
480			

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tgaggctcag ccctagccct cagcccacct ggggagtttta ctacctgggg accccccccttg 1671
cccatgcctc cagctacaaa acaattcaat tgctttttt ttttgtcca aaataaaacc 1731
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Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly Gly
35 40 45

Leu Gly Gly Tyr Gly Ala Ser Gly Met Gly Gly Ile Thr Ala
50 55 60

Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val Asp
65 70 75 80

Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys Thr
85 90 95

Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu Glu
100 105 110

Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln Gln
115 120 125

Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile Asn
130 135 140

Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys Leu
145 150 155 160

Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys Asn
165 170 175

Lys Tyr Glu Asp